

Figure 1

85P1B3 SSH sequence and GenBank homology to OIP5

GATCAGAGGACACATGGGACTCTGCATCTTAATTCCTAAATTTACAGTCAAAGACATTTTCAG
AGATAAGTATTATGAATTCAATAAGAATCTAAAGTAAGTTCTTAAGGCAAATAGCTATAAAA
GAGAAGAATCCTTAGTCTCTCATCTTCTAAAAACAGCTTCACAAATAATTTGGAAAATCAGCC
TAAAGGTAAATAGAACTGCATTTCCCTCCATTCTTGAAGCCAATCTTTTCAAGAAATGAC
TAAGCAGCACCTGTTGTTGAAGACAGCAATAAAGCCTGAACCTGACACTCAAGCTTTGGTACA
GGATC

gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein... 632 e-179
gb|AF158642.1|AF158642 Homo sapiens metalloproteinase-disin... 42 0.12
gb|AC005075.2|AC005075 Homo sapiens clone RG219E16, complet... 42 0.12
emb|AL096773.6|HS1000E10 Human DNA sequence from clone 1000... 40 0.48

>gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein OIP5 mRNA, partial cds
Length = 1197

Score = 632 bits (319), Expect = e-179
Identities = 319/319 (100%)
Strand = Plus / Minus

Query: 1 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacatttt 60
|||||
Sbjct: 1013 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacatttt 954

Query: 61 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaataagcta 120
|||||
Sbjct: 953 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaataagcta 894

Query: 121 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgga 180
|||||
Sbjct: 893 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgga 834

Query: 181 aatcagcctaaaggtaaataagaaactgcatttccctccattcttgaagccaatctttt 240
|||||
Sbjct: 833 aatcagcctaaaggtaaataagaaactgcatttccctccattcttgaagccaatctttt 774

Query: 241 caagaaatgactaagcagcacctgttgttgaagacagcaataaagcctgaacctgacact 300
|||||
Sbjct: 773 caagaaatgactaagcagcacctgttgttgaagacagcaataaagcctgaacctgacact 714

Query: 301 caagctttggtacaggatc 319
|||||
Sbjct: 713 caagctttggtacaggatc 695

Figure 2

cDNA Sequence and ORF of 85P1B3/OIP5 clone A

```

5'  GGC TGC GGG AAG ATG GCG GCT CAG CCG CTG CCG CAT CGC TCA CGT TGT GCA ACG
      9      18      27      36      45      54
      ---
      M  A  A  Q  P  L  R  H  R  S  R  C  A  T
      ---
      CCG CCC CGG GGG GAC TTT TGT GGT GGC ACT GAG AGG GCG ATT GAC CAA GCT TCT
      63      72      81      90      99      108
      ---
      P  P  R  G  D  F  C  G  G  T  E  R  A  I  D  Q  A  S
      ---
      TTT ACG ACC TCC ATG GAG TGG GAT ACG CAG GTG GTG AAG GGG TCC TCG CCG CTC
      117      126      135      144      153      162
      ---
      F  T  T  S  M  E  W  D  T  Q  V  V  K  G  S  S  P  L
      ---
      GGC CCC GCA GGG CTG GGG GCT GAG GAG CCA GCC GCC GGC CCG CAG CTG CCG TCT
      171      180      189      198      207      216
      ---
      G  P  A  G  L  G  A  E  E  P  A  A  G  P  Q  L  P  S
      ---
      TGG CTG CAG CCT GAG AGG TGC GCT GTG TTC CAG TGC GCA CAG TGT CAC GCA GTG
      225      234      243      252      261      270
      ---
      W  L  Q  P  E  R  C  A  V  F  Q  C  A  Q  C  H  A  V
      ---
      CTC GCC GAC TCG GTG CAC CTC GCC TGG GAC CTG TCG CGG TCC CTC GGG GCC GTG
      279      288      297      306      315      324
      ---
      L  A  D  S  V  H  L  A  W  D  L  S  R  S  L  G  A  V
      ---
      GTC TTC TCC AGA GTT ACA AAT AAC GTC GTT TTG GAA GCG CCC TTC CTA GTT GGC
      333      342      351      360      369      378
      ---
      V  F  S  R  V  T  N  N  V  V  L  E  A  P  F  L  V  G
      ---
      ATT GAA GGT TCA CTC AAA GGC AGT ACT TAC AAC CTT TTA TTC TGT GGT TCT TGT
      387      396      405      414      423      432
      ---
      I  E  G  S  L  K  G  S  T  Y  N  L  L  F  C  G  S  C
      ---
      GGG ATT CCC GTT GGT TTC CAT CTG TAT TCT ACC CAT GCT GCC CTG GCT GCC TTG
      441      450      459      468      477      486
      ---
      G  I  P  V  G  F  H  L  Y  S  T  H  A  A  L  A  A  L
      ---
      AGA GGT CAC TTC TGC CTT TCC AGT GAC AAA ATG GTG TGC TAT CTC TTA AAA ACA
      495      504      513      522      531      540
      ---
      R  G  H  F  C  L  S  S  D  K  M  V  C  Y  L  L  K  T
      ---
      AAA GCC ATA GTA AAT GCA TCA GAG ATG GAT ATT CAA AAT GTT CCT CTA TCA GAA
      549      558      567      576      585      594
      ---
      K  A  I  V  N  A  S  E  M  D  I  Q  N  V  P  L  S  E
      ---
      AAG ATT GCA GAG CTG AAA GAG AAG ATA GTG CTA ACG CAC AAT CGC TTA AAA TCA
      603      612      621      630      639      648
      ---
      K  I  A  E  L  K  E  K  I  V  L  T  H  N  R  L  K  S
  
```

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| | | | | | |
|---|------|------|------|------|------|
| 657 | 666 | 675 | 684 | 693 | 702 |
| CTA ATG AAG ATT CTG AGT GAA GTG ACT CCT GAC CAG TCC AAG CCA GAA AAC TGA | | | | | |
| L M K I L S E V T P D Q S K P E N * | | | | | |
| 711 | 720 | 729 | 738 | 747 | 756 |
| TCC TGT ACC AAA GCT TGA GTG TCA GGT TCA GGC TTT ATT GCT GTC TTC AAC AAC | | | | | |
| 765 | 774 | 783 | 792 | 801 | 810 |
| AGG TGC TGC TTA GTC ATT TCT TGA AAA AGA TTG GCT TCA AGA ATG GAG GGG AAA | | | | | |
| 819 | 828 | 837 | 846 | 855 | 864 |
| TGC AGT TTC TAT TTA CCT TTA GGC TGA TTT TCC AAA TTA TTT GTG AAG CTG TTT | | | | | |
| 873 | 882 | 891 | 900 | 909 | 918 |
| TTA GAA GAT GAG AGA CTA AGG ATT CTT CTC TTT TAT AGC TAT TTG CCT TAA GAA | | | | | |
| 927 | 936 | 945 | 954 | 963 | 972 |
| CTT ACT TTA GAT TCT TAT TGA ATT CAT AAT ACT TAT CTC TGA AAA TGT CTT TGA | | | | | |
| 981 | 990 | 999 | 1008 | 1017 | 1026 |
| CTG TAA ATT TAG GAA TTA AGA TGC AGA GTC CCA TGT GTC CTC TGA TCT AAA GTT | | | | | |
| 1035 | 1044 | 1053 | 1062 | 1071 | 1080 |
| GCA TGG TTG GTC TGA AAA TAG AGT TGG GCT TAA TGT TGA CTT CTA TTA CTC CTG | | | | | |
| 1089 | 1098 | 1107 | 1116 | 1125 | 1134 |
| CAT GGA GCA GTT GTT ATG AAT ACT AAT ACA TCA CTT TTT AAC TTC TGT AAA ATA | | | | | |
| 1143 | 1152 | 1161 | 1170 | 1179 | 1188 |
| CAG ATC ATA ATA TTC TAT AGG TAA TGT TTA ATA AAT TGC CTG AAT AAT AAA AAA | | | | | |
| 1197 | 1206 | 1215 | 1224 | 1233 | 1242 |
| AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA | | | | | |
| 1251 | 1260 | | | | |
| AAA AAA AAA AAA AAA AAA AA 3' | | | | | |

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Figure 3

85P1B3/OIP5 protein sequence.

1 MAAQPLRHRS RCATPPRGDF CGGTERAIDQ ASFTTSMEWD TQVVKGSSPL GPAGLGAEPP
61 AAGPQLPSWL QPERCAVFQC AQCHAVLADS VHLAWDLSRS LGAVVFSRVT NNVVLEAPFL
121 VGIEGSLKGS TYNLLFCGSC GIPVGFHLYS THAALAALRG HFCLSSDKMV CYLLKTKAIV
181 NASEMDIQNV PLSEKIAELK EKIVLTHNRL KSLMKILSEV TPDQSKPEN*

0044050930010823002504060

Figure 4

Alignment of 85P1B3 with OIP5.

>gi|2815610|gb|AAC39561.1| (AF025441) Opa-interacting protein OIP5 [Homo sapiens]
Length = 231

Score = 462 bits (1189), Expect = e-130
Identities = 229/229 (100%), Positives = 229/229 (100%)

```
85P1B3: 1  MAAQPLRHRSRCATPPRGDFCGGTERAIDQASF TTSMEWDTQVVKGSSPLGPAGLGAEFP 60
          MAAQPLRHRSRCATPPRGDFCGGTERAIDQASF TTSMEWDTQVVKGSSPLGPAGLGAEFP
OIP5: 3   MAAQPLRHRSRCATPPRGDFCGGTERAIDQASF TTSMEWDTQVVKGSSPLGPAGLGAEFP 62

85P1B3: 61  AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTNNVVLEAPFL 120
          AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTNNVVLEAPFL
OIP5: 63   AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTNNVVLEAPFL 122

85P1B3:121  VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 180
          VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV
OIP5: 123   VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 182

85P1B3:181  NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 229
          NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN
OIP5: 183   NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 231
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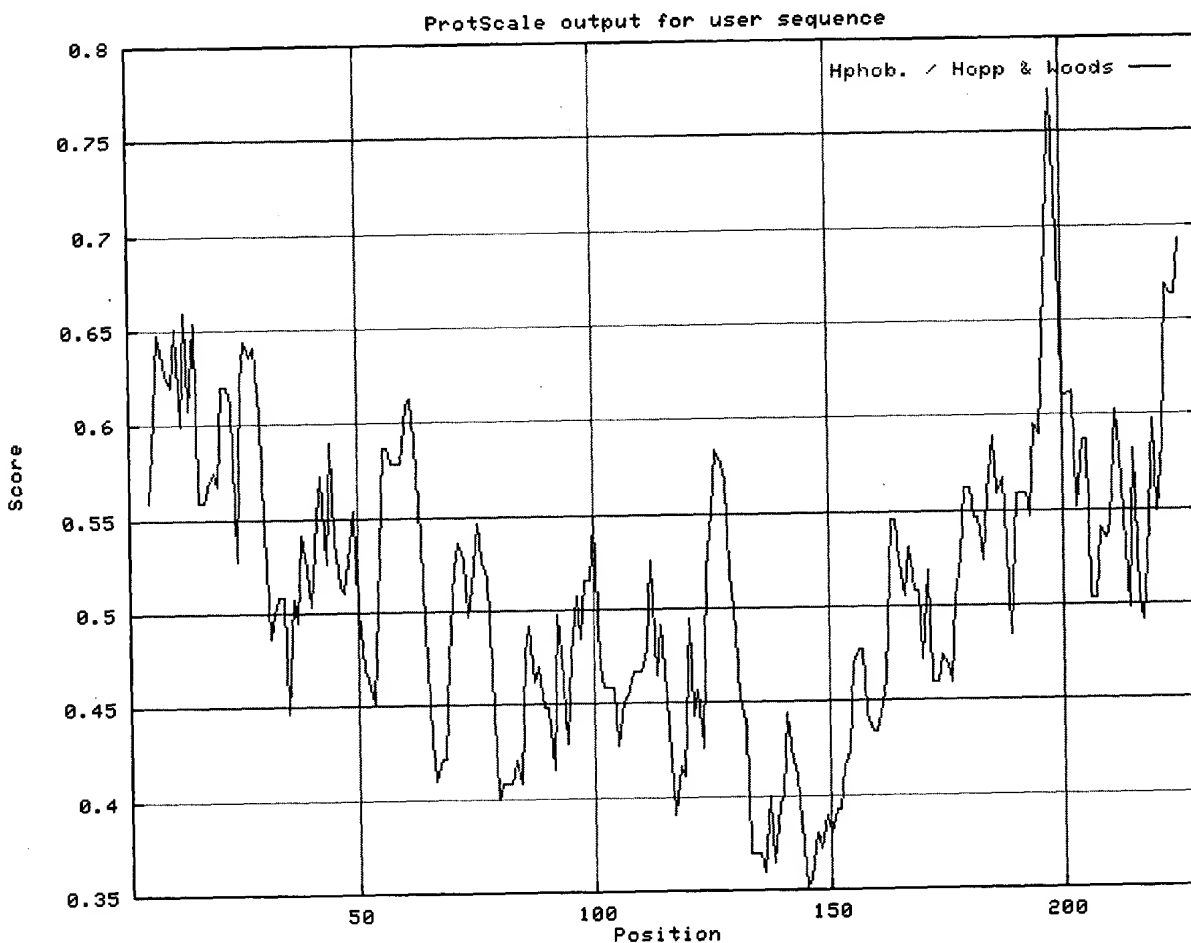
[illegible]

Figure 6: 85P1B3 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

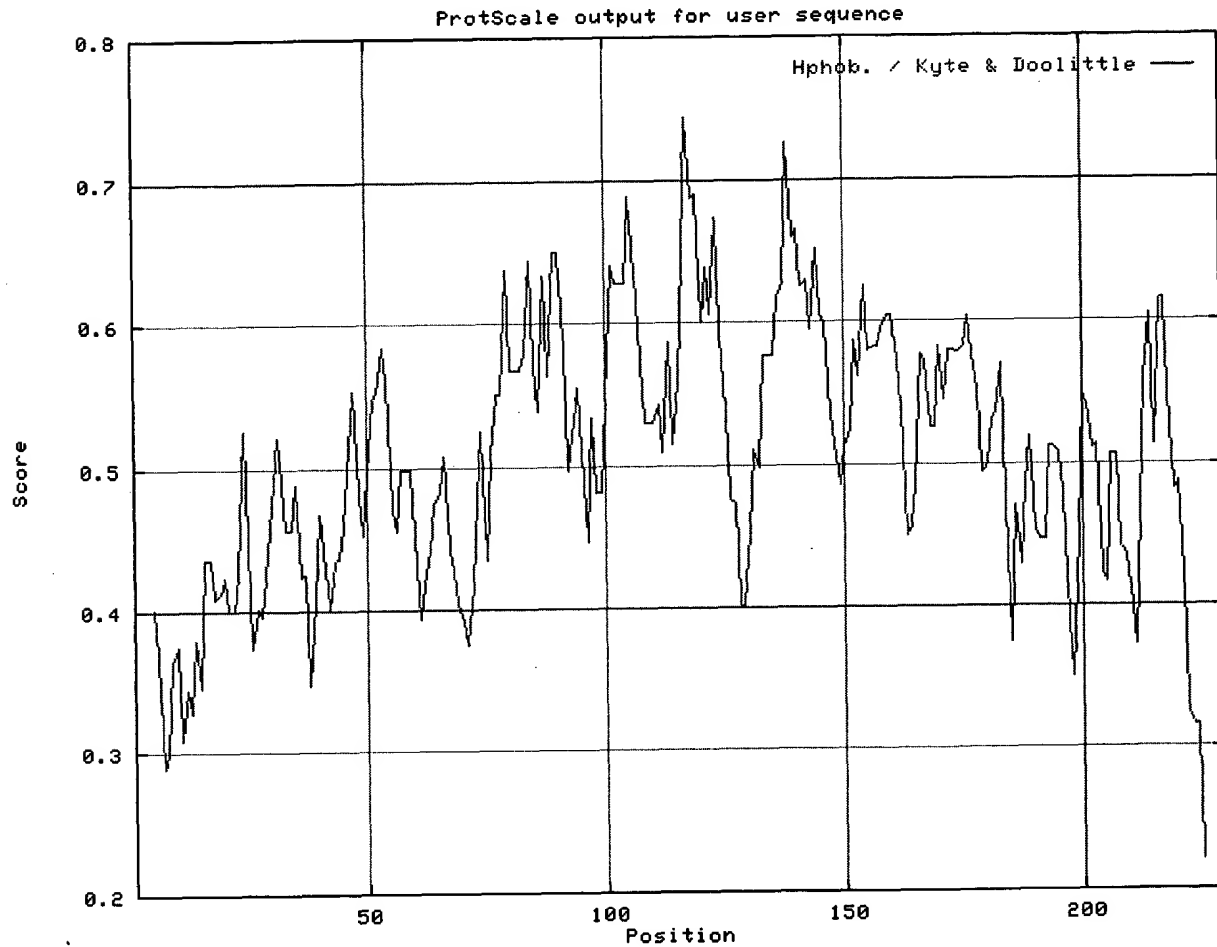


Figure 7: 85P1B3 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

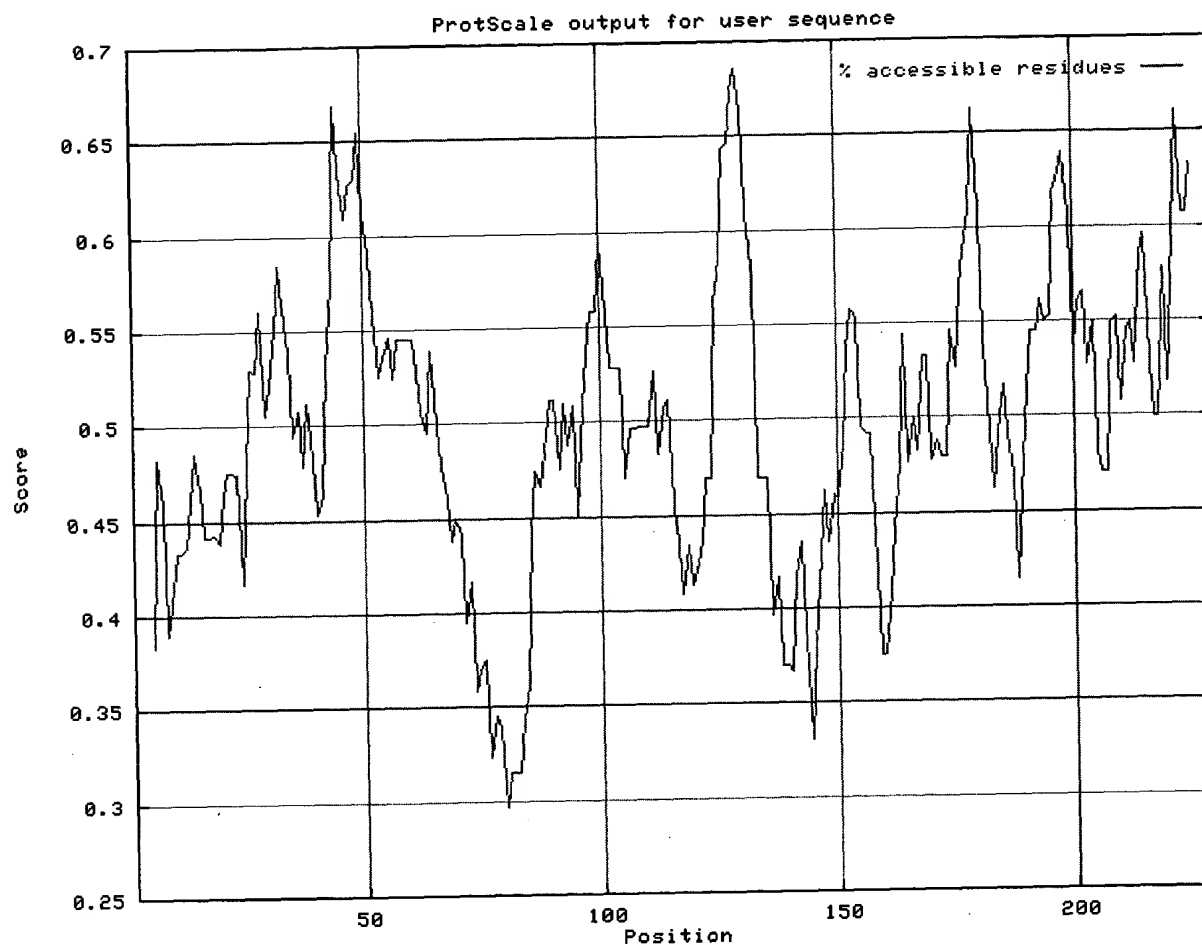
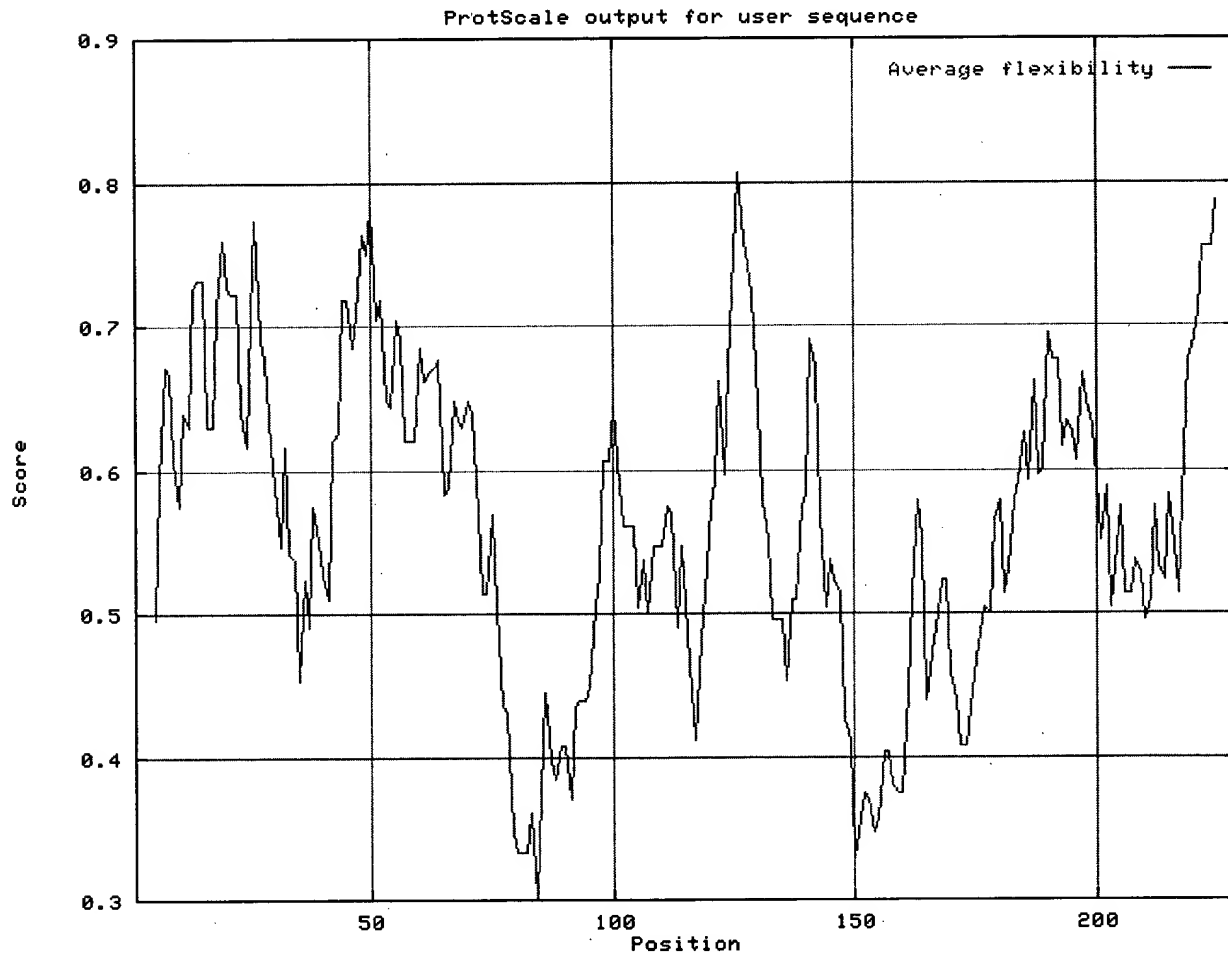


Figure 8: 85P1B3 Average Flexibility Profile

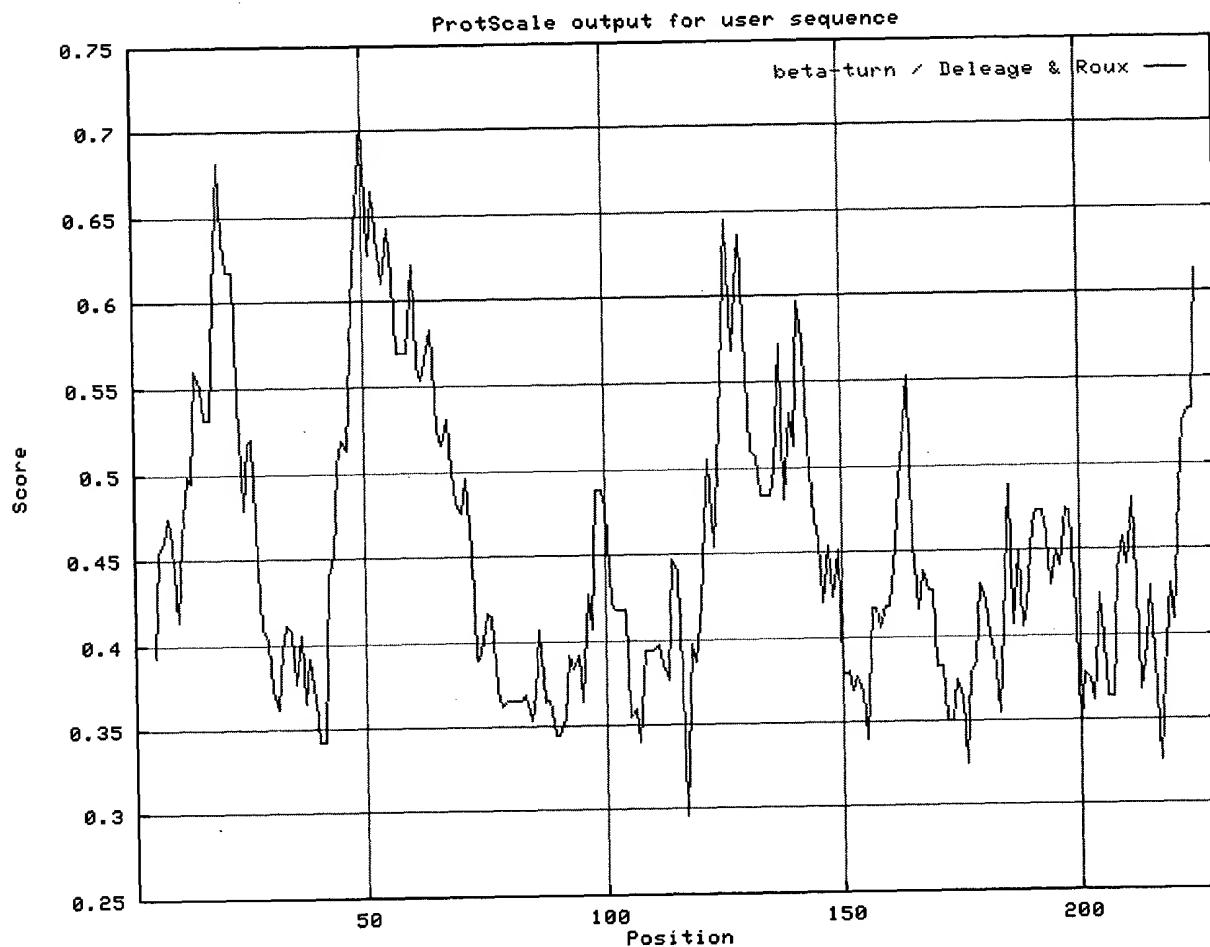
(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)



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Figure 9: 85P1B3 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)



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T08280" 25024660

Figure 10 RT-PCR analysis of 85P1B3 expression.

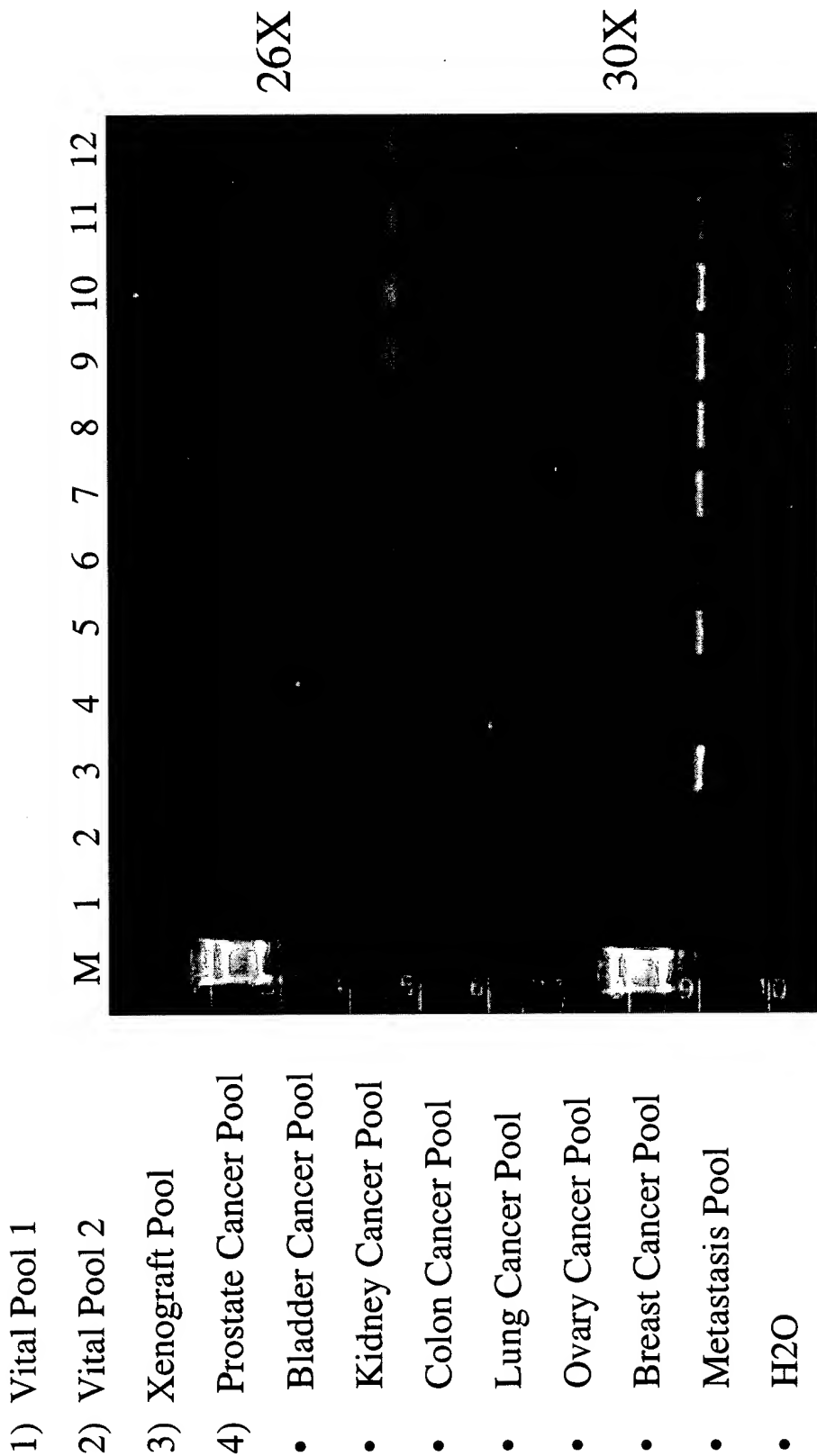


Figure 11 Expression of 85P1B3 in Normal Human Tissues

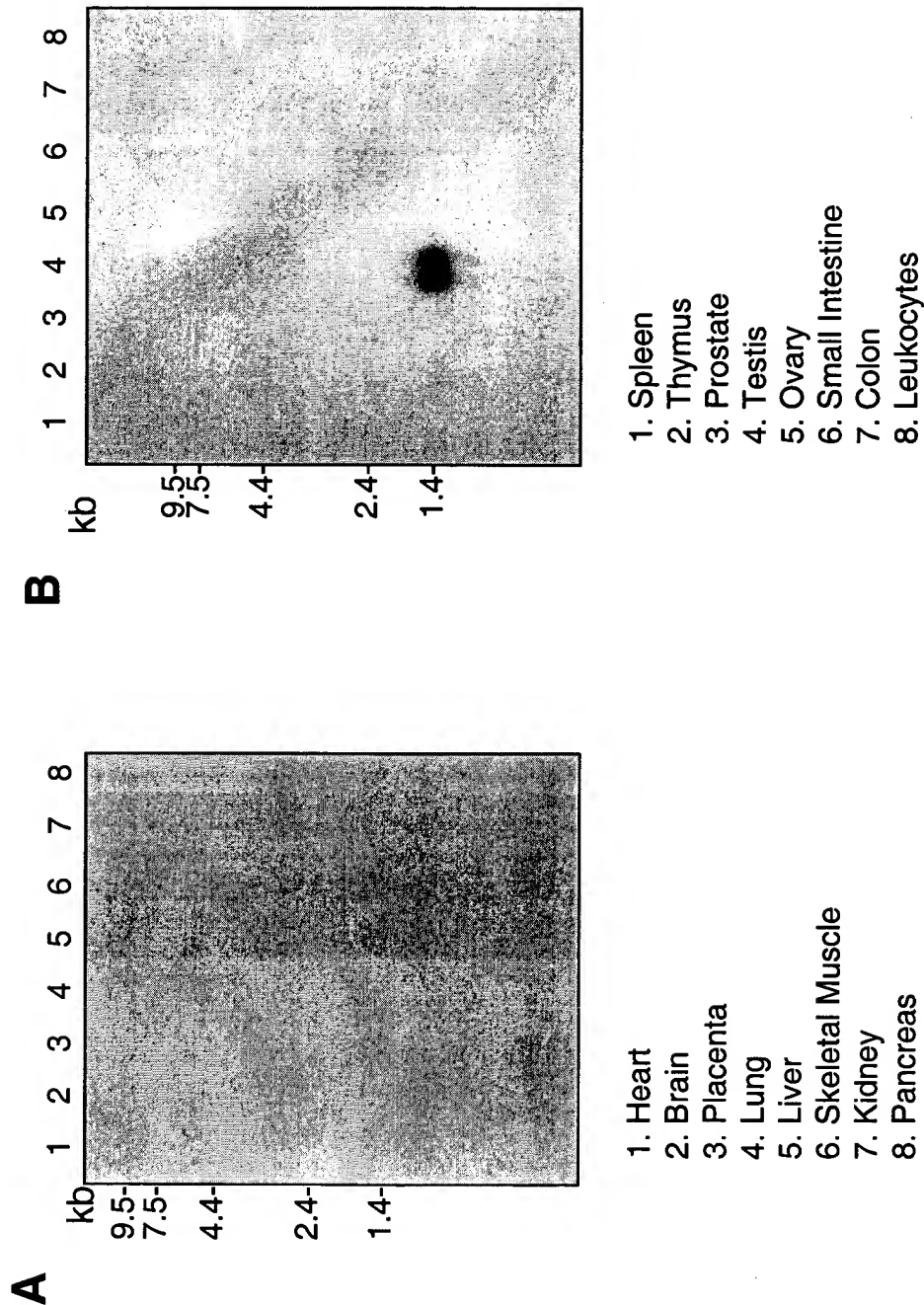


Figure 12 Expression of 85P1B3 in Human Cancer Cell lines

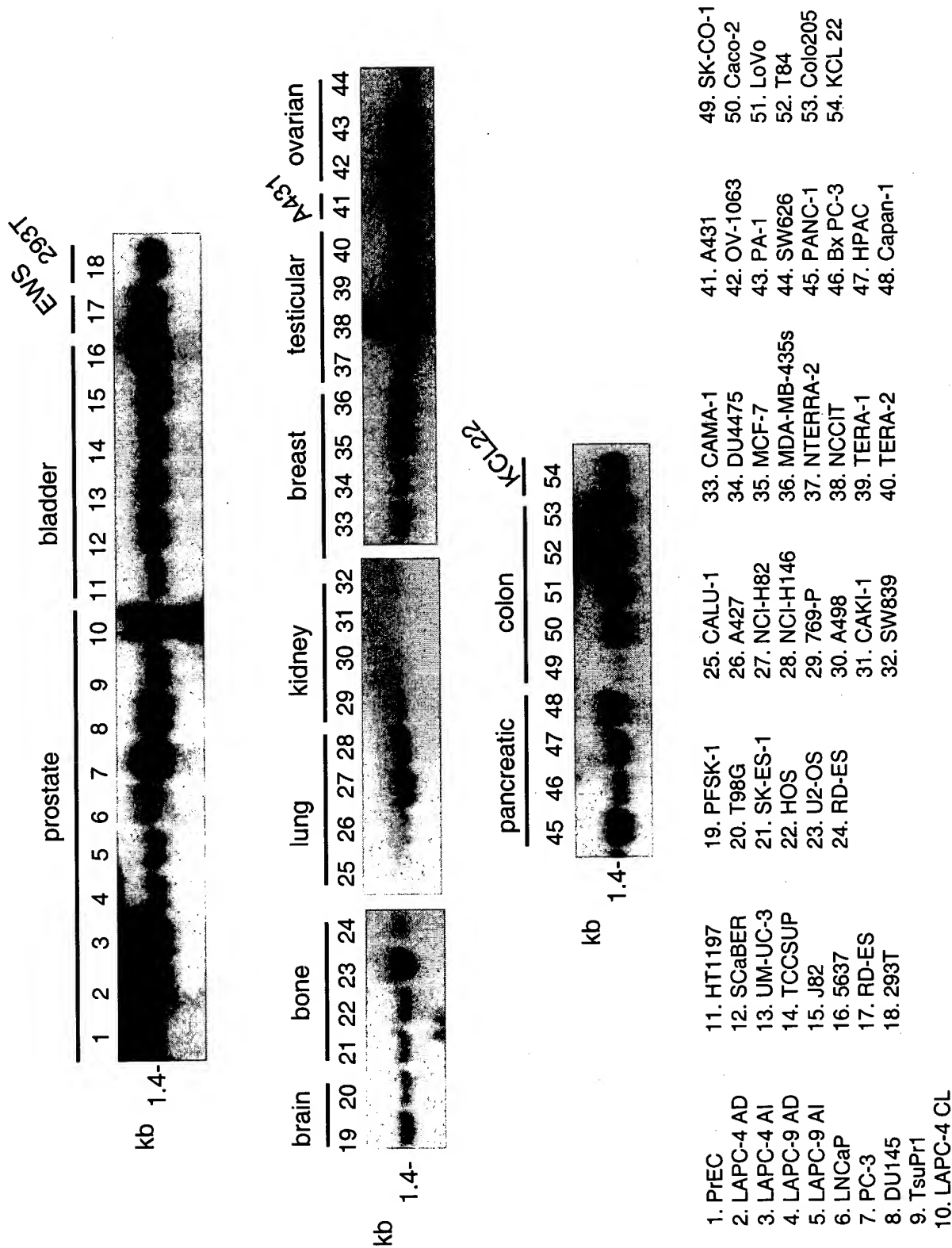


Figure 13 Expression of 85P1B3 in Patient Cancer Specimens and Cancer Cell Lines

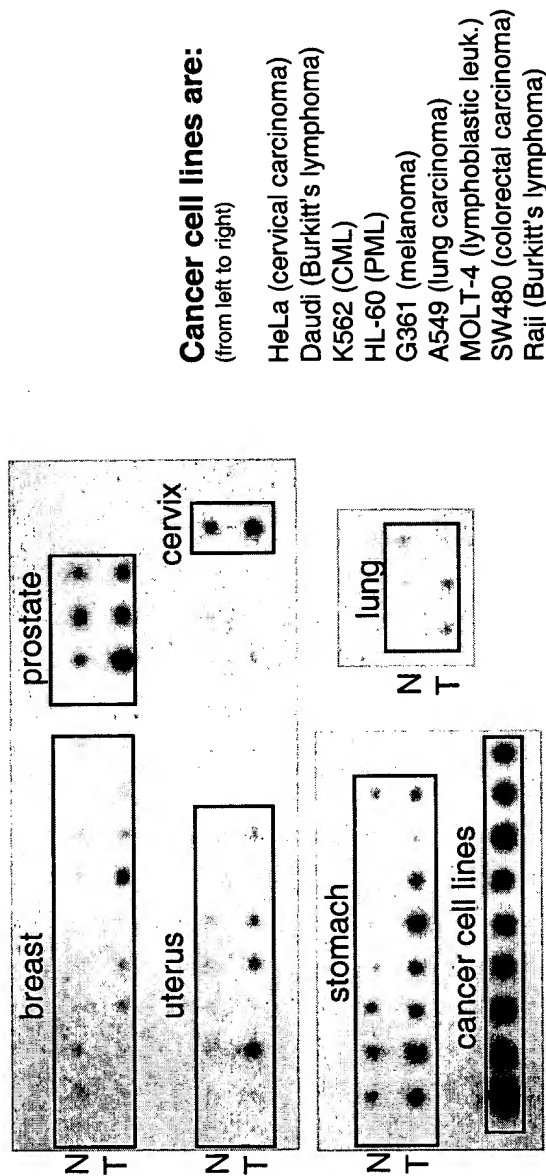


Figure 14 Expression of 85P1B3 in Colon Cancer Patient Specimens

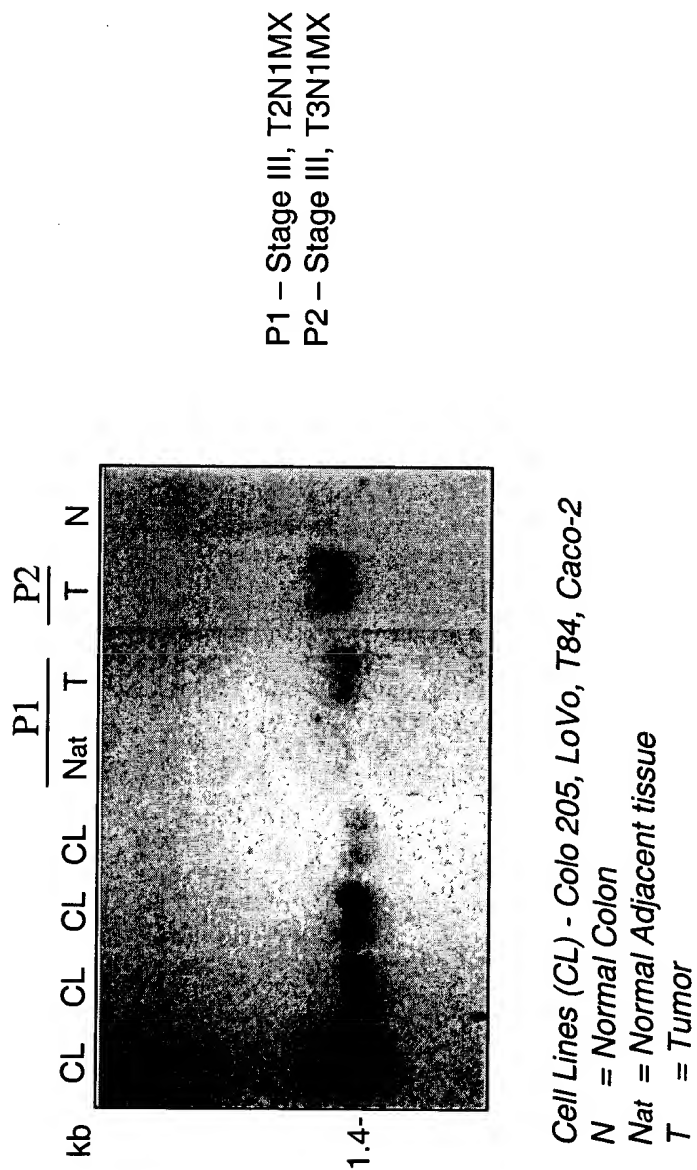
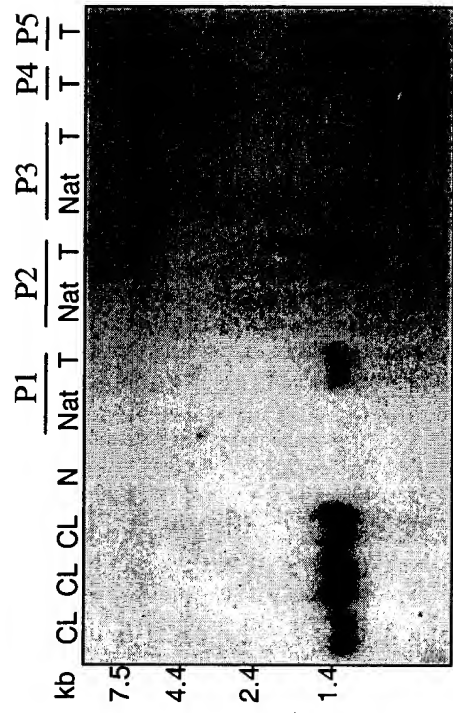


Figure 15 Expression of 85P1B3 in Bladder Cancer Patient Specimens



- P1 - Transitional, grade 2
- P2 - Transitional, grade 3/2
- P3 - Transitional
- P4 - Polypoid cystitis
- P5 - Papillary, grade 3

Cl = cell lines listed in order: UM-UC-3, J82, SCABER
P = Patient
N = Normal Bladder
Nat = Normal adjacent tumor
T = Tumor

Figure 16 Expression of 85P1B3 in Lung Cancer Patient Specimens

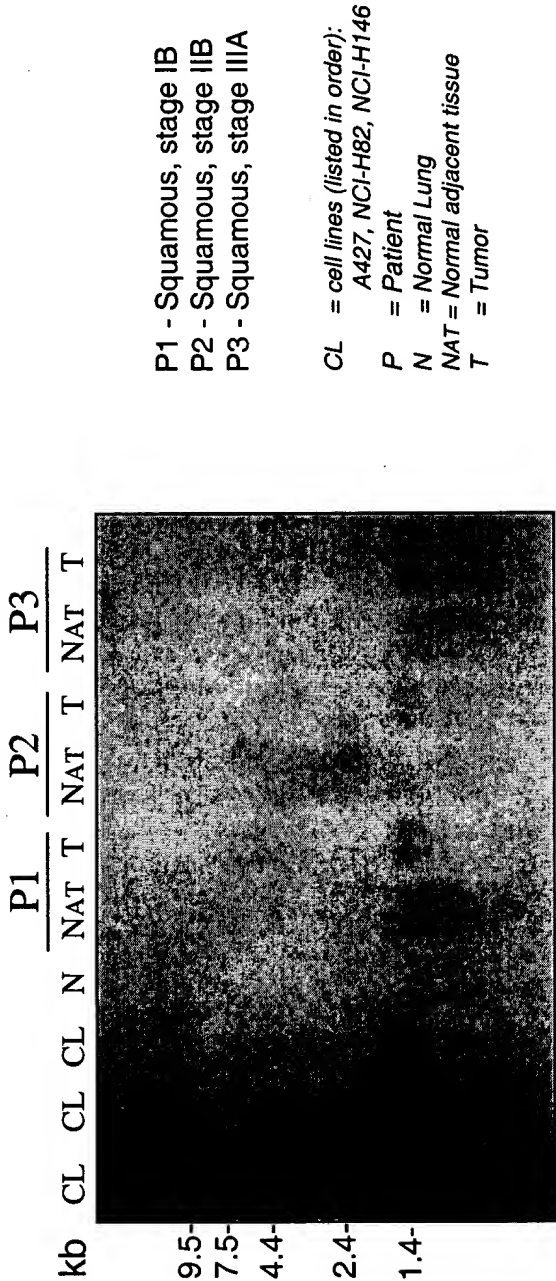


Figure 17 Expression of 85P1B3 in Prostate Cancer Xenografts Following Castration

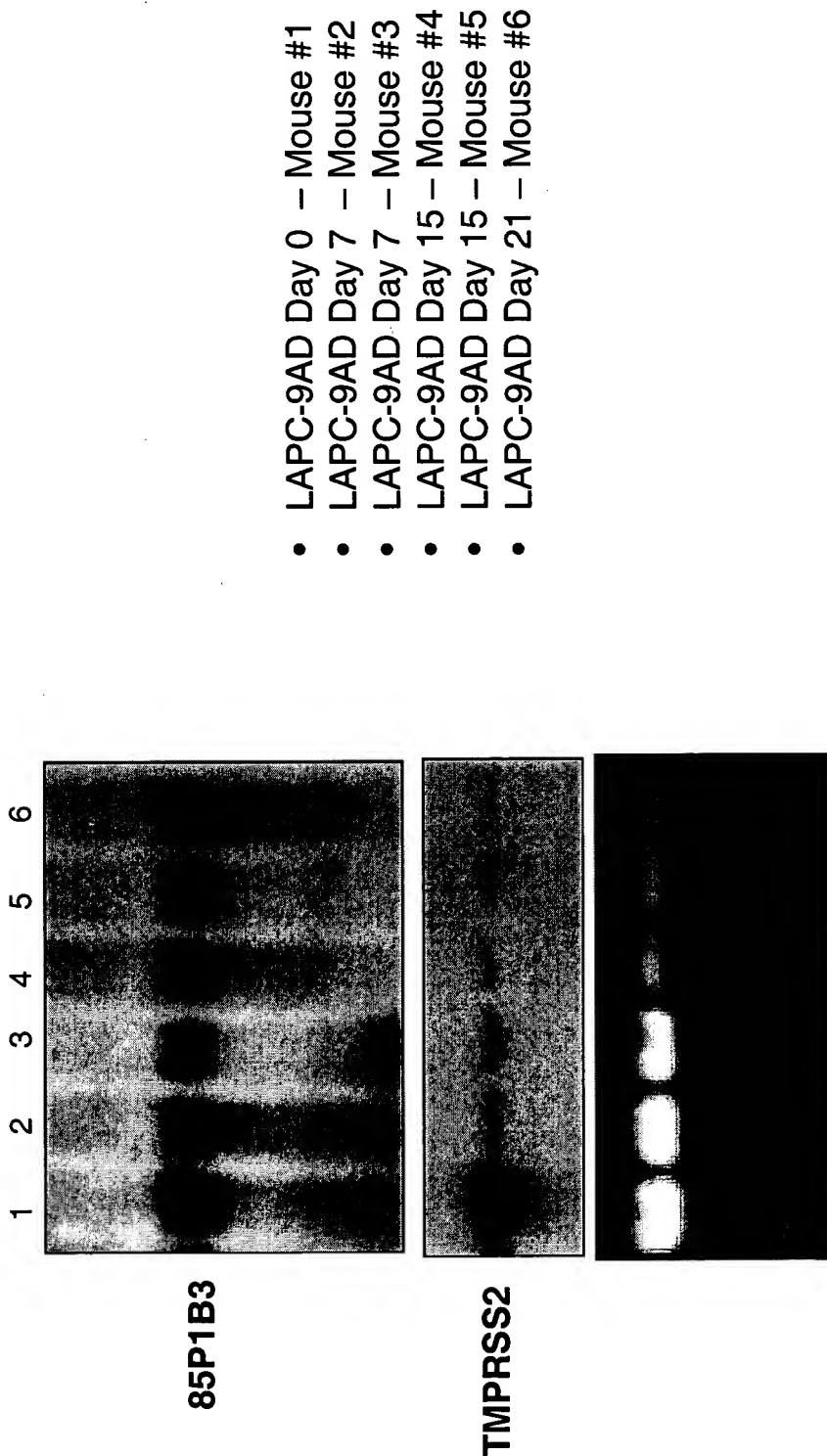


Figure 18 Expression of 85P1B3 in PC3 Cells Following Retroviral-Mediated Gene Delivery

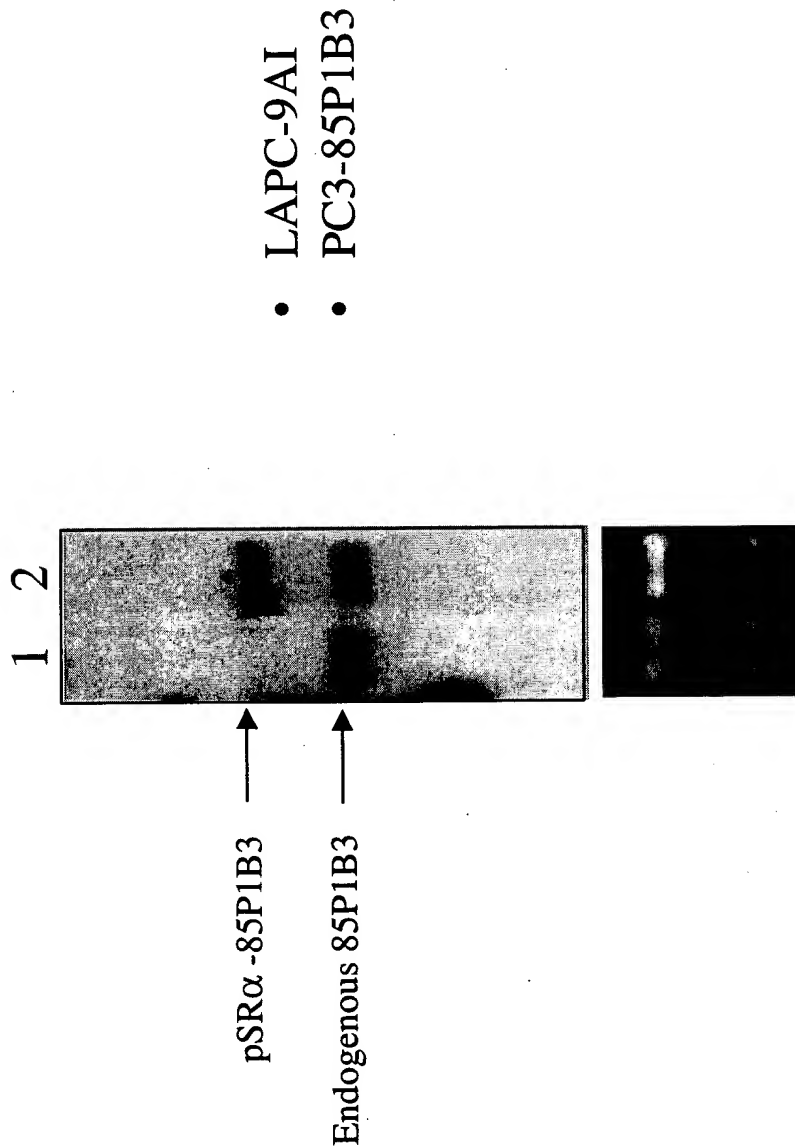
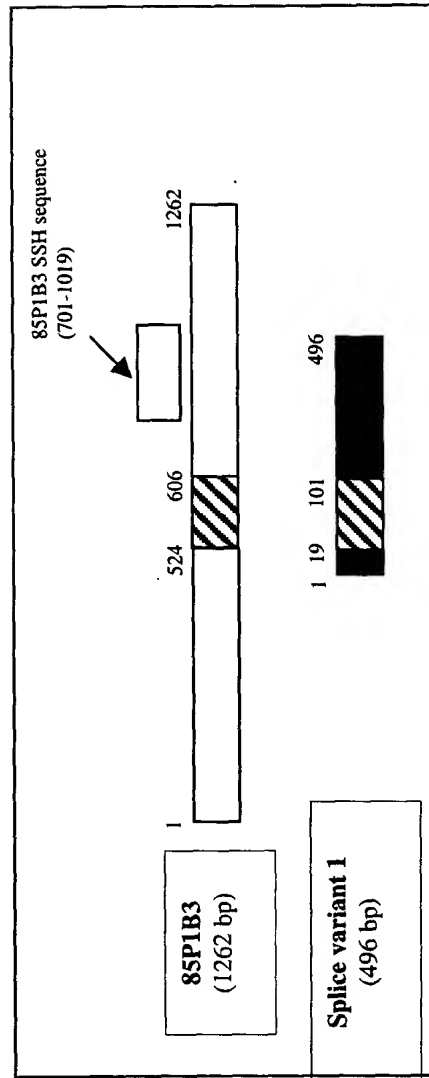
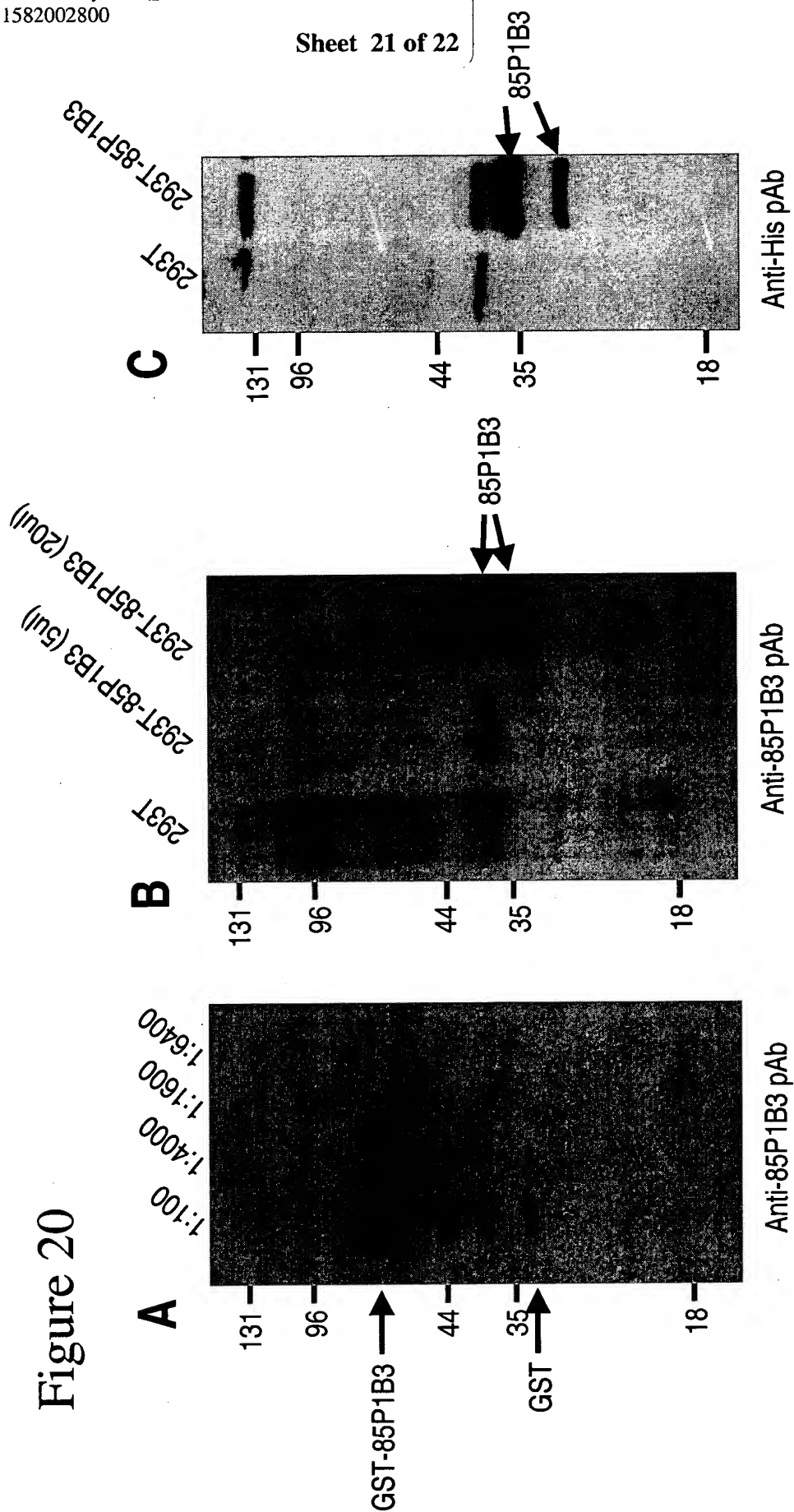


Figure 19.





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Fig. 21A

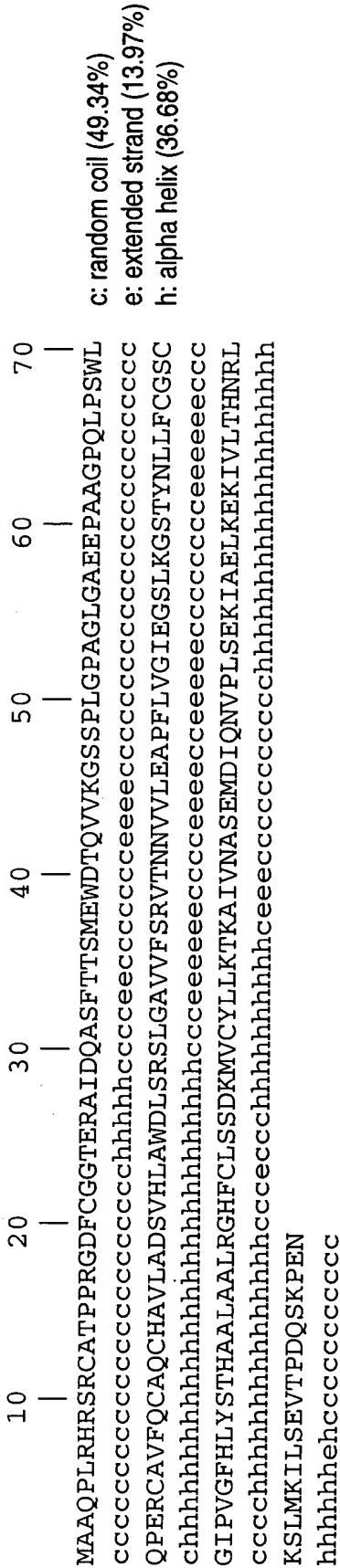
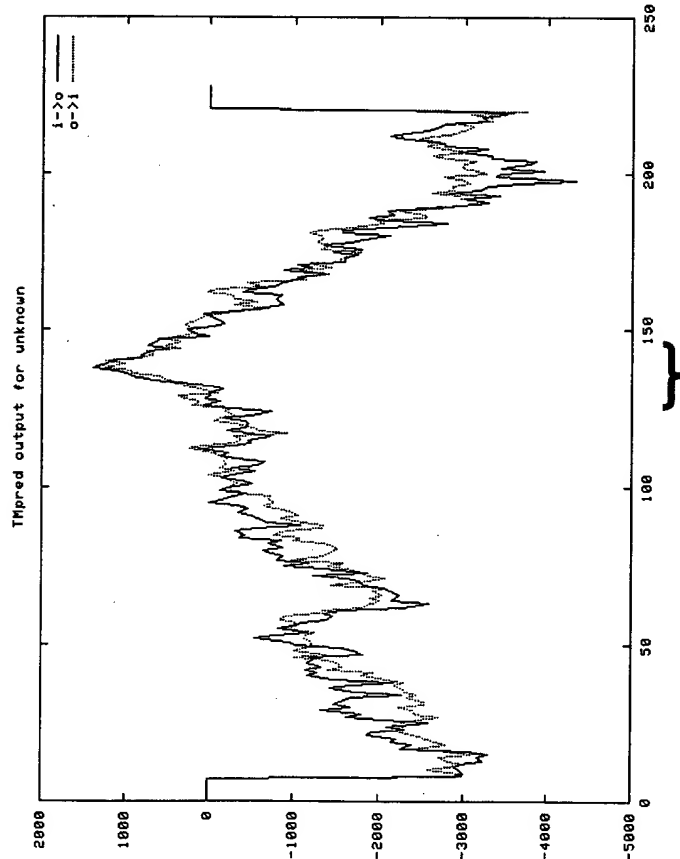
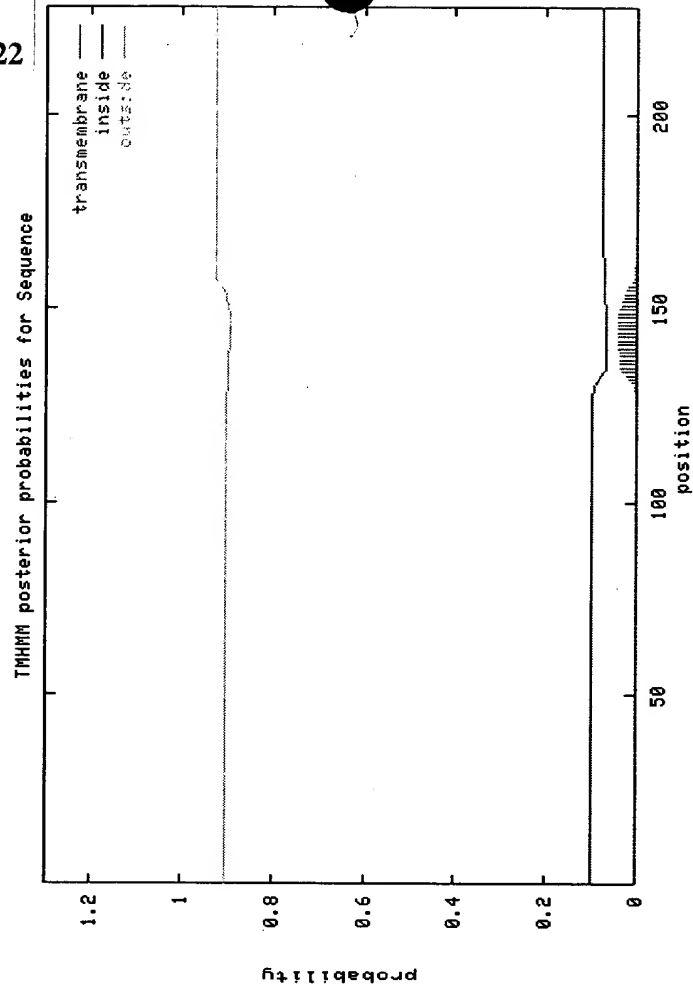


Fig. 21B



1 transmembrane from amino acids 129-149

Fig. 21C



No transmembrane domains, soluble protein